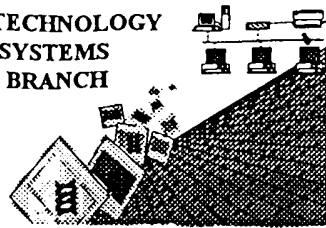


148E18, 1642

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/982,645  
Source: 1600  
Date Processed by STIC: 4/16/02

RECEIVED

APR 25 2002

TECH CENTER 1600/29

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 0000000000

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

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TECH CENTER 1000 2900



1600

Does Not Comply  
 Errors and Warnings Needed

## RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/982,645

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

3 <110> APPLICANT: CHEUNG, Nai-Kong V.  
 5 <120> TITLE OF INVENTION: USES OF MONOCLONAL ANTIBODY 8H9  
 7 <130> FILE REFERENCE: 638-B  
**C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/982,645**  
 10 <141> CURRENT FILING DATE: 2002-03-08  
 12 <150> PRIOR APPLICATION NUMBER: PCT/US01/32565  
 13 <151> PRIOR FILING DATE: 2001-10-18  
 15 <150> PRIOR APPLICATION NUMBER: 60/241,344  
 16 <151> PRIOR FILING DATE: 2000-10-18  
 18 <150> PRIOR APPLICATION NUMBER: 60/330,396  
 19 <151> PRIOR FILING DATE: 2001-10-17  
 21 <150> PRIOR APPLICATION NUMBER: 09/982,645  
 22 <151> PRIOR FILING DATE: 2001-10-18  
 24 <160> NUMBER OF SEQ ID NOS: 14  
 26 <170> SOFTWARE: PatentIn version 3.1  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 731  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: 8H9scfv cDNA sequence  
 33 <400> SEQUENCE: 1  
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 36 tcttgaacagg cttctggcta caccctcaca aactatgata taaactgggt gaggcagagg 120  
 38 cctgaacagg gacttgagtg gattggatgg attttctctg gagatggtag tactcaatac 180  
 40 aatgagaagt tcaagggcaa ggccacactg actacagaca catcctccag cacagcctac 240  
 42 atgcagctca gcaggtgac atctgaggac tctgtgtctc atttctgtgc aagacagact 300  
 44 acggctacct ggtttgctta ctggggccaa gggaccacgg tcaccgtctc ctcagatgga 360  
 46 ggcggttcag gcggaggtgg ctctggcggg ggcggatcgg acatcgagct cactcagtct 420  
 48 ccaaccaccc tgtctgtgac tccaggagat agagtctctc tttcctgcag ggccagccag 480  
 50 agtattagcg actacttaca ctggtaccaa caaaaatcac atgagtctcc aaggcttctc 540  
 52 atcaaatatg cttcccaatc catctctggg atccccctca ggttcagtgg cagtggatca 600  
 54 gggtcagatt tcactctcag tatcaacagt gtggaacctg aagatggttg agtgtattac 660  
 56 tgtcaaaatg gtcacagctt tccgctcacg ttcgggtgctg ggaccaagct ggagctgaaa 720  
 58 caggcggecg c 731  
 61 <210> SEQ ID NO: 2  
 62 <211> LENGTH: 243  
 63 <212> TYPE: PRT  
 64 <213> ORGANISM: 8H9scfv amino acid sequence  
 66 <400> SEQUENCE: 2  
 68 Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala  
 69 1 5 10 15  
 72 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
 73 20 25 30  
 76 Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,645

DATE: 04/16/2002

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

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77          35          40          45
80 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
81      50          55          60
84 Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Ser Thr Ala Tyr
85 65          70          75          80
88 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
89          85          90          95
92 Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
93          100          105          110
96 Thr Val Thr Val Ser Ser Asp Gly Gly Gly Ser Gly Gly Gly Ser
97      115          120          125
100 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr Thr Leu
101      130          135          140
104 Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln
105 145          150          155          160
108 Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser
109          165          170          175
112 Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro
113          180          185          190
116 Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile
117          195          200          205
120 Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly
121      210          215          220
124 His Ser Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
125 225          230          235          240
128 Gln Ala Ala
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 243
134 <212> TYPE: PRT
135 <213> ORGANISM: Mutated 8H9 scFv with decreased normal tissue adherence
137 <400> SEQUENCE: 3
139 Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
140 1          5          10          15
143 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
144          20          25          30
147 Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
148          35          40          45
151 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
152      50          55          60
155 Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Ser Thr Ala Tyr
156 65          70          75          80
159 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
160          85          90          95
163 Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
164          100          105          110
167 Thr Val Thr Val Ser Ser Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser
168          115          120          125
171 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr Thr Leu
172      130          135          140

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## RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/982,645

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

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175 Ser Val Thr Pro Gly Asp Gln Val Ser Leu Ser Cys Arg Ala Ser Gln
176 145                      150                      155                      160
179 Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser
180                      165                      170                      175
183 Pro Gln Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro
184                      180                      185                      190
187 Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile
188                      195                      200                      205
191 Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly
192      210                      215                      220
195 His Ser Phe Pro Leu Thr Phe Gly Ala Gly Thr Glu Leu Glu Leu Glu
196 225                      230                      235                      240
199 Gln Ala Ala
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 22
205 <212> TYPE: DNA
206 <213> ORGANISM: [32P]r Probe
208 <400> SEQUENCE: 4
209 tactctcagc agaacaccta tg                                22
212 <210> SEQ ID NO: 5
213 <211> LENGTH: 21
214 <212> TYPE: DNA
215 <213> ORGANISM: Primer: ESBP1
217 <400> SEQUENCE: 5
218 cgactagtta tgatcagagc a                                21
221 <210> SEQ ID NO: 6
222 <211> LENGTH: 23
223 <212> TYPE: DNA
224 <213> ORGANISM: Primer: ESBP2
226 <400> SEQUENCE: 6
227 ccgttgctct gtattcttac tga                                23
230 <210> SEQ ID NO: 7
231 <211> LENGTH: 18
232 <212> TYPE: DNA
233 <213> ORGANISM: Primer: EWS 696
235 <400> SEQUENCE: 7
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240 <211> LENGTH: 20
241 <212> TYPE: DNA
242 <213> ORGANISM: Primer: FLI 1 1041
244 <400> SEQUENCE: 8
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248 <210> SEQ ID NO: 9
249 <211> LENGTH: 25
250 <212> TYPE: DNA
251 <213> ORGANISM: Primer: G6PD1
253 <400> SEQUENCE: 9
254 ccggatcgac cactacctgg gcaag                                25

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,645

DATE: 04/16/2002

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

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257 <210> SEQ ID NO: 10
258 <211> LENGTH: 26
259 <212> TYPE: DNA
260 <213> ORGANISM: Primer: G6PD2
262 <400> SEQUENCE: 10
263 gttccccacg tactggccca ggacca
266 <210> SEQ ID NO: 11
267 <211> LENGTH: 24
268 <212> TYPE: DNA
269 <213> ORGANISM: Lightcycler Hybridization Probe: EWSHP1
271 <400> SEQUENCE: 11
272 tatagccaac agagcagcag ctac
275 <210> SEQ ID NO: 12
276 <211> LENGTH: 18
277 <212> TYPE: DNA
278 <213> ORGANISM: Lightcycler Hybridization Probe: EWSHP2
280 <400> SEQUENCE: 12
281 ggcagcagaa cccttctt
284 <210> SEQ ID NO: 13
285 <211> LENGTH: 28
286 <212> TYPE: DNA
287 <213> ORGANISM: Lightcycler Hybridization Probe: G6PDHP1
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290 gttccagatg gggccgaaga tctgttg
293 <210> SEQ ID NO: 14
294 <211> LENGTH: 28
295 <212> TYPE: DNA
296 <213> ORGANISM: Lightcycler Hybridization Probe: G6PDHP2
298 <400> SEQUENCE: 14
299 caaatctcag caccatgagg ttctgcac

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/982,645

DATE: 04/16/2002

TIME: 14:31:43

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number